AMENDMENTS TO THE CLAIMS:

The claims as currently presented and under consideration, are presented below for the Examiner's convenience and to comply with 37 CFR §1.121:

1. (Previously presented): A method of increasing the secretion of a heterologous protein in a eukaryotic cell comprising inducing an elevated unfolded protein response (UPR) by increasing the presence of a UPR-modulating protein isolated from a yeast or a filamentous fungi, wherein said UPR-modulating protein comprises a DNA binding domain that has at least 70% similarity to a DNA binding domain set forth in Figure 10, and further wherein the induction of the elevated UPR results in the increased secretion of the heterologous protein relative to the parental cell.

2. (Original): The method of Claim 1 wherein inducing is by increasing the presence of HAC1 protein in said cell.

3. (Original): The method of Claim 2 wherein said HAC1 protein is constitutively produced.

4. (Original): The method of Claim 2 wherein said increase of HAC1 protein is by a UPR inducing form of a HAC1 recombinant nucleic acid.

5. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from a cell selected from the group consisting of *Aspergillus, Trichoderma, Saccharomyces, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Fusarium, Neurospora,* and *Penicillium.*

6. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from yeast.

7. (Original): The method of Claim 6 wherein said yeast is *Saccharomyces cerevisiae.*

8. (Original): The method of Claim 2 wherein said HAC1 protein is encoded by a nucleic acid isolated from filamentous fungi.

9. (Original): The method of Claim 8 wherein said fungi is from *Trichoderma*.

10. (Original): The method of Claim 8 wherein said fungi is *Trichoderma reesei*.

11. (Original): The method of Claim 8 wherein said fungi is from *Aspergillus*.

12. (Original): The method of Claim 8 wherein said fungi is *Aspergillus nidulans*.

13. (Original): The method of Claim 8 wherein said fungi is *Aspergillus niger*.

14- 25. (Cancelled)

26. (Original): The method of Claim 1 wherein said cell is selected from the group consisting of *Aspergillus, Trichoderma, Saccharomyces, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Fusarium, Neurospora,* and *Penicillium*.

27. (Original): The method of Claim 1 wherein said cell is a yeast cell.

28. (Original): The method of Claim 27 wherein said yeast is *Saccharomyces cerevisiae*.

29. (Currently amended): The method of Claim 1 wherein said cell is a ~~from~~ filamentous fungi.

30. (Original): The method of Claim 29 wherein said fungi is from *Trichoderma*.

31. (Original): The method of Claim 29 wherein said fungi is *Trichoderma reesei*.

32. (Original): The method of Claim 29 wherein said fungi is from *Aspergillus*.

33. (Original): The method of Claim 29 wherein said fungi is *Aspergillus nidulans*.

34. (Original): The method of Claim 29 wherein said fungi is *Aspergillus niger*.

35. (Cancelled) The method of Claim 1 wherein said cell is an insect cell.

36. (Original): The method of Claim 1 wherein said cell is a mammalian cell.

37-82. (Cancelled)

83. (Withdrawn) A cell containing a heterologous nucleic acid encoding a yeast or filamentous fungi protein having unfolded protein response modulating activity and a heterologous nucleic

acid encoding a protein of interest to be secreted.

84. (Withdrawn): The cell of Claim 83 wherein said protein having unfolded protein response modulating activity is a fungal HAC1.

85. (Withdrawn): The cell of Claim 83 wherein said protein of interest is selected from the group consisting of lipase, cellulase, endo-glucosidase H, protease, carbohydrase, reductase, oxidase, isomerase, transferase, kinase, phosphatase, alpha-amylase, glucoamylase, ligtnocellulose hemicellulase, pectinase and ligninase.

86. (Cancelled)

87. (Withdrawn): The cell of Claim 83 wherein said protein having unfolded protein response modulating activity is a yeast HAC1.

88. (New): The method of Claim 1 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 80% similarity to a DNA binding domain set forth in Figure 10.

89. (New): The method of Claim 1 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 90% similarity to a DNA binding domain set forth in Figure 10.

90. (New): The method of Claim 1 wherein said UPR-modulating protein comprises a DNA binding domain that has at least 95% similarity to a DNA binding domain set forth in Figure 10.

91. (New): The method of Claim 1 wherein said UPR-modulating protein comprises a DNA binding domain having the DNA binding domain of amino acid residue positions 84 to 147 of SEQ ID NO: 5.

92. (New): The method of Claim 1 wherein said UPR-modulating protein comprises a DNA binding domain having the DNA binding domain of amino acid residue positions of 53 to 116 of SEQ ID NO: 6.

93. (New): The method of Claim 1, wherein said heterologous protein is selected from the group consisting of lipases, cellulases, endo-glucosidase H, proteases, carbohydrases,

reductases, oxidases, isomerases, transferases, kinases, phosphatases, alpha-amylases, glucoamylases, hemicellulases, pectinases and ligninases.

94. (New): The method of Claim 93, wherein the heterologous protein is a protease, cellulase, glucoamylase or alpha amylase.

95. (New): The method of Claim 1, wherein the eukaryotic cell is a Trichoderma or Aspergillus fungal cell, the UPR-modulating protein comprising a DNA binding domain has at least 90% sequence similarity to a DNA binding domain set forth in Figure 10 and the heterologous protein is selected from the group of proteases, cellulase, glucoamylase, alpha amylases and combination thereof.